

1/23

GAATTCGGCTTCATCCTAATACGACTCACTATAGGGCTCGAGCGGCCCGCCGGGGCAGGTATCTTGGCTCACAGGGGA 79

M S S S S W L L L S L V A V T A A Q S 19
CG ATG TCA AGC TCT TCC TGG CTC CTT CTC AGC CTT GTT GCT GTA ACT GCT GCT CAG TCC 138

T I E E Q A K T F L D K F N H E A E D L 39
ACC ATT GAG GAA CAG GCC AAG ACA TTT TTG GAC AAG TTT AAC CAC GAA GCC GAA GAC CTG 198

F Y Q S S L A S W N Y N T N I T E E N V 59
TTC TAT CAA AGT TCA CTT GCT TCT TGG AAT TAT AAC ACC AAT ATT ACT GAA GAG AAT GTC 258

Q N M N N A G D K W S A F L K E Q S T L 79
CAA AAC ATG AAT AAT GCT GGG GAC AAA TGG TCT GCC TTT TTA AAG GAA CAG TCC ACA CTT 318

A Q M Y P L Q E I Q N L T V K L Q L Q A 99
GCC CAA ATG TAT CCA CTA CAA GAA ATT CAG AAT CTC ACA GTC AAG CTT CAG CTG CAG GCT 378

L Q Q N G S S V L S E D K S K R L N T I 119
CTT CAG CAA AAT GGG TCT TCA GTG CTC TCA GAA GAC AAG AGC AAA CGG TTG AAC ACA ATT 438

L N T M S T I Y S T G K V C N P D N P Q 139
CTA AAT ACA ATG AGC ACC ATC TAC AGT ACT GGA AAA GTT TGT AAC CCA GAT AAT CCA CAA 498

E C L L L E P G L N E I M A N S L D Y N 159
GAA TGC TTA TTA CTT GAA CCA GGT TTG AAT GAA ATA ATG GCA AAC AGT TTA GAC TAC AAT 558

E R L W A W E S W R S E V G K Q L R P L 179
GAG AGG CTG TGG GCT TGG GAA AGC TGG AGA TCT GAG GTC GGC AAG CAG CTG AGG CCA TTA 618

Y E E Y V V L K N E M A R A N H Y E D Y 199
TAT GAA GAG TAT GTG GTC TTG AAA AAT GAG ATG GCA AGA GCA AAT CAT TAT GAG GAC TAT 678

G D Y W R G D Y E V N G V D G Y D Y S R 219
GGG GAT TAT TGG AGA GGA GAC TAT GAA GTA AAT GGG GTA GAT GGC TAT GAC TAC AGC CGC 738

G Q L I E D V E H T F E E I K P L Y E H 239
GGC CAG TTG ATT GAA GAT GTG GAA CAT ACC TTT GAA GAG ATT AAA CCA TTA TAT GAA CAT 798

L H A Y V R A K L M N A Y P S Y I S P I 259
CTT CAT GCC TAT GTG AGG GCA AAG TTG ATG AAT GCC TAT CCT TCC TAT ATC AGT CCA ATT 858

G C L P A H L L G D M W G R F W T N L Y 279
GGA TGC CTC CCT GCT CAT TTG CTT GGT GAT ATG TGG GGT AGA TTT TGG ACA AAT CTG TAC 918

S L T V P F G Q K P N I D V T D A M V D 299
TCT TTG ACA GTT CCC TTT GGA CAG AAA CCA AAC ATA GAT GTT ACT GAT GCA ATG GTG GAC 978

Q A W D A Q R I F K E A E K F F V S V G 319
CAG GCC TGG GAT GCA CAG AGA ATA TTC AAG GAG GCC GAG AAG TTC TTT GTA TCT GTT GGT 1038

L P N M T Q G F W E N S M L T D P G N V 339
CTT CCT AAT ATG ACT CAA GGA TTC TGG GAA AAT TCC ATG CTA ACG GAC CCA GGA AAT GTT 1098

Q K A V C H P T A W D L G K G D F R I L 359
CAG AAA GCA GTC TGC CAT CCC ACA GCT TGG GAC CTG GGG AAG GGC GAC TTC AGG ATC CTT 1158

M C T K V T M D D F L T A H H E M G H I 379
ATG TGC ACA AAG GTG ACA ATG GAC GAC TTC CTG ACA GCT CAT CAT GAG ATG GGG CAT ATC 1218 ZBD

Q Y D M A Y A A Q P F L L R N G A N E G 399
CAG TAT GAT ATG GCA TAT GCT GCA CAA CCT TTT CTG CTA AGA AAT GGA GCT AAT GAA GGA 1278

F H E A V G E I M S L S A A T P K H L K 419
TTC CAT GAA GCT GTT GGG GAA ATC ATG TCA CTT TCT GCA GCC ACA CCT AAG CAT TTA AAA 1338

S I G L L S P D F Q E D N E T E I N F L 439
TCC ATT GGT CTT CTG TCA CCC GAT TTT CAA GAA GAC AAT GAA ACA GAA ATA AAC TTC CTG 1398

L K Q A L T I V G T L P F T Y M L E K W 459
CTC AAA CAA GCA CTC ACG ATT GTT GGG ACT CTG CCA TTT ACT TAC ATG TTA GAG AAG TGG 1458

R W M V F K G E I P K D Q W M K K W W E 479
AGG TGG ATG GTC TTT AAA GGG GAA ATT CCC AAA GAC CAG TGG ATG AAA AAG TGG TGG GAG 1518

Fig. 1A

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M K | intron 9 R E I V G V V E P V P H D E T Y C D 499
ATG AAG CGA GAG ATA GTT GGG GTG GTG GAA CCT GTG CCC CAT GAT GAA ACA TAC TGT GAC 1578

P A S L F H V S N D Y S F I R | intron 10 Y Y T R T 519
CCC GCA TCT CTG TTC CAT GTT TCT AAT GAT TAC TCA TTC ATT CGA TAT TAC ACA AGG ACC 1638

L Y Q F Q F Q E A L C Q A A K H E G F L 539
CTT TAC CAA TTC CAG TTT CAA GAA GCA CTT TGT CAA GCA GCT AAA CAT GAA GGC CCT CTG 1698

H K C D I S N S T E A G Q K L | intron 11 F N M L R 559
CAC AAA TGT GAC ATC TCA AAC TCT ACA GAA GCT GGA CAG AAA CTG TTC AAT ATG CTG AGG 1758

L G K S E P W T L A L E N V V G A K N M 579
CTT GGA AAA TCA GAA CCC TGG ACC CTA GCA TTG GAA AAT GTT GTA GGA GCA AAG AAC ATG 1818

N V R P L L N Y F E P L F T W L K D Q N 599
AAT GTA AGG CCA CTG CTC AAC TAC TTT GAG CCC TTA TTT ACC TGG CTG AAA GAC CAG AAC 1878

K N S F V G W S T D W S E | intron 12 Y A D Q S I K 619
AAG AAT TCT TTT GTG GGA TGG AGT ACC GAC TGG AGT CCA TAT GCA GAC CAA AGC ATC AAA 1938

V R I S L K S A L G D K A | intron 13 Y E W N D N E 639
GTG AGG ATA AGC CTA AAA TCA GCT CTT GGA GAT AAA GCA TAT GAA TGG AAC GAC AAT GAA 1998

M Y L F R S S V A Y A M R Q Y F L K V K 659
ATG TAC CTG TTC CGA TCA TCT GTT GCA TAT GCT ATG AGG CAG TAC TTT TTA AAA GTA AAA 2058

N O M I L F G | intron 14 E E D V R V A N L K P R I 679
AAT CAG ATG ATT CTT TTT GGG GAG GAG GAT GTG CGA GTG GCT AAT TTG AAA CCA AGA ATC 2118

S F N F F V T A P K N V S D I I F R T E 699
TCC TTT AAT TTC TTT GTC ACT GCA CCT AAA AAT GTG TCT GAT ATC ATT CCT AGA ACT GAA 2178

V E K A I R | intron 15 M S R S R I N D A F R L N D 719
GTT GAA AAG GCC ATC AGG ATG TCC CGG AGC CGT ATC AAT GAT CCT TTC CGT CTG AAT GAC 2238

N S L E F L G I Q P T L G P P N O P F V 739
AAC AGC CTA GAG TTT CTG GGG ATA CAG CCA ACA CTT GGA CCT CCT AAC CAG CCC CCT GTT 2298

S | I W L I V F G V V M G V I V V G I V I 759
TCC ATA TGG CTG ATT GTT TTT GGA GTT GTG ATG GGA GTG ATA GTG GTT GGC ATT GTC ATC 2358 TMD

L I F T G I | intron 16 R D R K K K N K A R S G E N 779
CTG ATC TTC ACT GGG ATC AGA GAT CGG AAG AAG AAA AAT AAA GCA AGA AGT GGA GAA AAT 2418

P Y A S I D I S K G E N N P G F Q N T D 799
CCT TAT GCC TCC ATC GAT ATT AGC AAA GGA GAA AAT AAT CCA GGA TTC CAA AAC ACT GAT 2478

D V Q T S F * 806
GAT GTT CAG ACC TCC TTT TAG 2499

AAAAATCTATGTTTTTCTCTTGAGGTGATTTTGTGTATGTAAATGTTAATTTTCATGGTATAGAAAAATATAAGATGAT 2578
AAAGATATCATTAAATGTCAAAACTATGACTCTGTTTCAGAAAAAAATTTGTCGAAAGACAACATGGCCAAGGAGAGAGC 2657
ATCTTCATTGACATTGCTTTTCACTATTTATTTCTGTCTCTGGATTGACTTCTGTTCTGTTTCTTAATAAGGATTTTGT 2736
ATTAGAGTATATTAGGGAAAGTGTGTATTTGGTCTCACAGGCTGTTTCAGGGATAATCTAAATGTAAATGTCTGTTGAAT 2815
TTCTGAAGTTGAAAAACAAGGATATATCATTTGGAGCAAGTGTGGATCTTGTATGGAATATGGATGGATCACTTGTAAAG 2894
ACAGTGCCTGGGAAGTGGTGTAGCTGCAAGGATTGAGAATGGCATGCATTAGCTCACTTTTCATTTAATCCATTGTCAAG 2973
GATGACATGCTTTTCTTCACAGTAACCTCAGTTCAAGTACTATGGTGATTTGCCTACAGTGATGTTTGAATCGATCATGC 3052
TTTCTTCAAGGTGACAGGTCTAAAGAGAGAAGAATCCAGGGAACAGGTAGAGGACATTGCTTTTTTCACTTCCAAGGTGC 3131
TTGATCAACATCTCCCTGACAACACAAAACCTAGAGCCAGGGGCTCCGTGAACCTCCAGAGCATGCCTGATAGAACTC 3210
ATTTCTACTGTTCTCTAACTGTGGAGTGAATGGAAATFCCAACCTGTATGTTCCACCTCTGAAGTGGGTACCCAGTCTCT 3289
TAAATCTTTTGTATTTGCTCACAGTGTGAGCAGTGCTGAGCACAAAGCAGACACTCAATAAATGCTAGATTTACACA 3368
CTCAAAAAAAAAAAAAAGGGCGGCCGC 3396

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Fig. 1B

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ace-2 -----
hu-ACET -----
mu-ACET -----
rb-ACET -----
hu-ACE MGAASGRRGPGLLLPLP-----LLLLL-PPQFALALDPGLQPGNFSADEAGAQLFAQSYN
mu-ACE MGAASGQGRWPLSPPLLMLSLLVLLLQP-SPAPA;DPGLQPGNFSPPDEAGAQLFAESYN
rat-ACE MGAASGQGRWPLSPPLLMLSLLLLLLLLPPSPAPALDPGLQPGNFSADEAGAQLFADSYN
rb-ACE MGAAPGRRGPRLLRPPPL-LLLLLLRPPPAALTLDPLGLPGDFAADEAGARLFASSYN

ace-2 -----
hu-ACET -----
mu-ACET -----
rb-ACET -----
hu-ACE SSAEQVLFQSVASWAHDTNITAENARRQEEAALLSQEFAEAWGQKAKELYEPIWQNFDT
mu-ACE SSAEVVMFQSTVASWAHDTNITEENARRQEEAALVSQEFAEVWGKAKELYESIWNQNFDT
rat-ACE SSAEVVMFQSTAASWAHDTNITEENARLQEEAALINQEFAEVWGKAKELYESIWNQNFDT
rb-ACE SSAEQVLFIRSTAASWAHDTNITAENARRQEEAALLSQEFAEAWGRRLRSSMTRCGRTSFT

ace-2 -----
hu-ACET -----
mu-ACET -----
rb-ACET -----
hu-ACE POLRRIIGAVRTLGSANLPLAKRQYNALLSNMSRIYSTAKVCLPNKTATCWSLDPDLTN
mu-ACE SKLRRIIGSIRTLGPANLPLAQROQYNALLSNMSRIYSTGKVCFPNKTATCWSLDPDLTN
rat-ACE OKLRRIIGSVQTLGFANLPLTORLQYNALLSNMSRIYSTGKVCFPNKTATCWSLDPDLTN
rb-ACE QSCAGSSGLCAFWPCQAP-GQAAADNSLLSNMSQIYSTGRSASPTPLPAAWSLDPDLNN

ace-2 -----
hu-ACET -----
mu-ACET -----
rb-ACET -----
hu-ACE ILASSRSYAMLLFAWEGWHNAAGIPLKPLYEDFTALSNEAYKQDGFSDTGAYWRSWYNP
mu-ACE ILASSRSYAKLLFAWEGWHDVGIPLKPLYQDFTALSNEAYRQDDFSDTGAFWRSWYESP
rat-ACE ILASSRNYAKVLFWEGWHDVGIPLRPLYQDFTALSNEAYRQDGFSDTGAYWRSWYESP
rb-ACE ILASSRSYAMLLFAWEGWHNAVGIPLKPLYQDFTALSNEAYRQDGFSDTGAYWRSWYDSP

ace-2 -----
hu-ACET -----
mu-ACET -----
rb-ACET -----
hu-ACE TFEDDLEHLYQOLEPLYLNLHAFVRRALHRRYGDRIYNLRGPIPAHLLGDMWAQSWENIY
mu-ACE SFEEBLEHLYHQLEPLYLNLHAYVRRALHRRYGDRIYNLRGPIPAHLLGDMWAQSWENIY
rat-ACE SFEEBLEHLYHQVEPLYLNLHAFVRRALHRRYGDRIYNLRGPIPAHLLGDMWAQSWENIY
rb-ACE TFEDLERIYHQLEPLYLNLHAYVRRVLRHRRYGDRIYNLRGPIPAHLLGNMWAQSWESIY

ace-2 -----
hu-ACET -----
mu-ACET -----
rb-ACET -----
hu-ACE DMVVPFPDKPNLDVTSTMVQKGNATHMFRVAEEFFTSLELSPMPPEFWEGSMLEKPADG
mu-ACE DMVVPFPDKPNLDVTSTMVQKGNATHMFRVSEEFFTSLELSPMPPEFWAESMLEKPTDG
rat-ACE DMVVPFPDKPNLDVTSTMVQKGNATHMFRVAEEFFTSLELSPMPPEFWAESMLEKPADG
rb-ACE DMVVPFPDKPNLDVTSTMVQKGNATHMFRVAEEFFTSLELSPMPPEFWAESMLEKPEDG

ace-2 -----
hu-ACET -----
mu-ACET -----
rb-ACET -----
hu-ACE REVVCHASAWDFYNRKDFRIKQCTRVMTDQLSTVHHEMGHVQYLYQKDLVSLRRGANP
mu-ACE REVVCHASAWDFYNRKDFRIKQCTRVMTDQLSTVHHEMGHVQYLYQKDLVSLRRGANP
rat-ACE REVVCHASAWDFYNRKDFRIKQCTRVMTDQLSTVHHEMGHVQYLYQKDLVSLRRGANP
rb-ACE REVVCHASAWDFYNRKDFRIKQCTQVTMDQLSTVHHEMGHVQYLYQKDPVSLRR-ANP

Fig. 2A

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ace-2      NGVDGYDYSRGOLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAY-PSYISPIGCLPAHLLG
hu-ACET    P-----SLEQDLERLFOELOPLYLNLHAYVRRALHRHYGAQHINLEGPIPAHLLG
mu-ACET    D-----NLEQDLEKLYQELOPLYLNLHAYVRRSLHRHYGSEYINLDGPIPAHLLG
rb-ACET    P-----TLEQDLERLFOELOPLYLNLHAYVGRALHRHYGAQHINLEGPIPAHLLG
hu-ACE     P-----SLEQDLERLFOELOPLYLNLHAYVRRALHRHYGAQHINLEGPIPAHLLG
mu-ACE     D-----NLEQDLEKLYQELOPLYLNLHAYVRRSLHRHYGSEYINLDGPIPAHLLG
rat-ACE    D-----DLEQDLEKLYQELOPLYLNLHAYVRRSLHRHYGSEYINLDGPIPAHLLG
rb-ACE     P-----TLEQDLERLFOELOPLYLNLHAYVGRALHRHYGAQHINLEGPIPAHLLG
           * :*: :*: :*: :*: :*: :* . * .*: * :*****

ace-2      DMWGRFWTNLYSLTVFPGOKPNIDVTDAMVDOAWDAQRIFKEAEKFFVSVGLPNMTQGF
hu-ACET    NMWAQTWSNIYDLVVPFPPSAPSMDTTEAMLKQGWTPRRMFKEADFFFTSLGLLPVPPEFW
mu-ACET    NMWAQTWSNIYDLVAPFPPSAPNIDATEAMIKQGWTPRRIFKEADNFFFTSLGLLPVPPEFW
rb-ACET    NMWAQTWSNIYDLVAPFPPSASTMDATEAMIKQGWTPRRMFKEADKFFISLGLLPVPPEFW
hu-ACE     NMWAQTWSNIYDLVVPFPPSAPSMDTTEAMLKQGWTPRRMFKEADFFFTSLGLLPVPPEFW
mu-ACE     NMWAQTWSNIYDLVAPFPPSAPNIDATEAMIKQGWTPRRIFKEADNFFFTSLGLLPVPPEFW
rat-ACE    NMWAQTWSNIYDLVAPFPPSAPSIDATEAMIKQGWTPRRIFKEADNFFFTSLGLLPVPPEFW
rb-ACE     NMWAQTWSNIYDLVAPFPPSASTMDATEAMIKQGWTPRRMFKEADKFFISLGLLPVPPEFW
           :*: :*: :*: :*: :*: :* .*: :*: :*: :* :*: :*

ace-2      ENSMLTDPGNVQKAVCHPTAWDLGKG-DFRILMCTKVMTDDFLTAHHEMGGHIQYDMAYAA
hu-ACET    NKSMLEKPTDGREVVCHASAWDFYNGKDFRIKQCTTVNLEDLVVAHHEMGGHIQYFMQYKD
mu-ACET    NKSMLEKPTDGREVVCHPSAWDFYNGKDFRIKQCTSVNMEDLVIAHHEMGGHIQYFMQYKD
rb-ACET    NKSMLEKPTDGREVVCHASAWDFYNGKDFRIKQCTTVNMEDLVVHHEMGGHIQYFMQYKD
hu-ACE     NKSMLEKPTDGREVVCHASAWDFYNGKDFRIKQCTTVNLEDLVVAHHEMGGHIQYFMQYKD
mu-ACE     NKSMLEKPTDGREVVCHPSAWDFYNGKDFRIKQCTSVNMEDLVIAHHEMGGHIQYFMQYKD
rat-ACE    NKSMLEKPTDGREVVCHASAWDFYNGKDFRIKQCTSVNMEELVIAHHEMGGHIQYFMQYKD
rb-ACE     NKSMLEKPTDGREVVCHASAWDFYNGKDFRIKQCTTVNMEDLVVHHEMGGHIQYFMQYKD
           :*: :* : :*: :*: :*: :* :* :*: :* :*: :* :*

ace-2      QPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSLIGLLSPDFQEDNETEINFLKQALTIV
hu-ACET    LPVALREGANPGFHEAIGDVLALSVSTPKHLHSLNLLSSEGGSD-EHDINFLMKMALDKI
mu-ACET    LPVTFREGANPGFHEAIGDIMALSVSTPKHLHSLNLLSTEGSGY-EYDINFLMKMALDKI
rb-ACET    LPVALREGANPGFHEAIGDVLALSVSTPKHLHSLNLLSSEGGGY-EHDINFLMKMALDKI
hu-ACE     LPVALREGANPGFHEAIGDVLALSVSTPKHLHSLNLLSSEGGSD-EHDINFLMKMALDKI
mu-ACE     LPVTFREGANPGFHEAIGDIMALSVSTPKHLHSLNLLSTEGSGY-EYDINFLMKMALDKI
rat-ACE    LPVTFREGANPGFHEAIGDVLALSVSTPKHLHSLNLLSSEGGGY-EHDINFLMKMALDKI
rb-ACE     LPVALREGANPGFHEAIGDVLALSVSTPKHLHSLNLLSSEGGGY-EHDINFLMKMALDKI
           * . :*: :* :*: :*: :*: :* :*: :* :* :* :* :*

ace-2      GTLPFTYMLEKWRWVFKGEIPKDQWMKKWEMKREIVGVVEPVPHDETYCDPASLFHVS
hu-ACET    AFIPFSYLVDQWRWRVFDGSITKENYNQEWWSLRLKYQGLCPPVPRTOGDFDPGAKFHIP
mu-ACET    AFIPFSYLIDQWRWRVFDGSITKENYNQEWWSLRLKYQGLCPPVPRSQGDFDPGSKFHVP
rb-ACET    AFIPFSYLVDQWRWRVFDGSITKENYNQEWWSLRLKYQGLCPPAPRSQGDFDPGAKFHIP
hu-ACE     AFIPFSYLVDQWRWRVFDGSITKENYNQEWWSLRLKYQGLCPPVPRTOGDFDPGAKFHIP
mu-ACE     AFIPFSYLIDQWRWRVFDGSITKENYNQEWWSLRLKYQGLCPPVPRSQGDFDPGSKFHVP
rat-ACE    AFIPFSYLIDQWRWRVFDGSITKENYNQEWWSLRLKYQGLCPPVPRSQGDFDPGSKFHVP
rb-ACE     AFIPFSYLVDQWRWRVFDGSITKENYNQEWWSLRLKYQGLCPPAPRSQGDFDPGAKFHIP
           . :*: :*: :*: :*: :*: :* :* :* :* :* :* :*

ace-2      NDYSFIRYYTRTLYQFQFQALCOAAKHEGPLHKCDISNSTEAGOKLFNMLRLGKSEPWT
hu-ACET    SSVPIRYFVVSFIIQFQFHEALCOAGHTGPLHKCDIYQSKEAGQRLATAMKLGFSRPWP
mu-ACET    ANVPYVRYFVVSFIIQFQFHEALCRAAGHTGPLHKCDIYQSKEAGKLLADAMKLGYSKPWP
rb-ACET    SSVPIRYFVVSFIIQFQFHEALCKAAGHTGPLHTCDIYQSKEAGKRLADAMKLGYSKPWP
hu-ACE     SSVPIRYFVVSFIIQFQFHEALCOAGHTGPLHKCDIYQSKEAGQRLATAMKLGFSRPWP
mu-ACE     ANVPYVRYFVVSFIIQFQFHEALCRAAGHTGPLHKCDIYQSKEAGKLLADAMKLGYSKPWP
rat-ACE    ANVPYIRYFISFIIQFQFHEALCRAAGHTGPLYKCDIYQSKEAGKLLADAMKLGYSKQWP
rb-ACE     SSVPIRYFVVSFIIQFQFHEALCKAAGHTGPLHTCDIYQSKEAGKRLADAMKLGYSKPWP
           . :*: :* : :*: :*: :*: :* :* :* :* :* :* :*

ace-2      LALENVVGAKNMNVRLNLYFEPLFTWLKDONKNSFVGWSTDWSPYADQSIKVRISLKSA
hu-ACET    EAMQLITGQPNMSASAMLSYFKPLLDWLRTENEL-----HGEK
mu-ACET    EAMKLITGQPNMSASAMNLYFKPLTEWLVTENRR-----HGET
rb-ACET    EAMKVITGQPNMSASAMNLYFKPLMDWLLTENGR-----HGEK
hu-ACE     EAMQLITGQPNMSASAMLSYFKPLLDWLRTENEL-----HGEK
mu-ACE     EAMKLITGQPNMSASAMNLYFKPLTEWLVTENRR-----HGET
rat-ACE    EAMKIITGQPNMSASAIMNLYFKPLTEWLVTENRR-----HGET
rb-ACE     EAMKVITGQPNMSASAMNLYFKPLMDWLLTENGR-----HGEK
           *: :* :* :* :* :* :* :* :* :* :* :* :*
```

Fig. 2C

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ace-2	LGDKAYEWNDNEMYLFRRSSVAYAMRQYFLKVKNQMILFGEEDVRVANLKPRI SFNFFVTA
hu-ACET	LGWPQYNWTPN-----
mu-ACET	LGWPEYNWAPN-----
rb-ACET	LGWPQYTWTPN-----
hu-ACE	LGWPQYNWTPN-----
mu-ACE	LGWPEYNWAPN-----
rat-ACE	LGWPEYTWTPN-----
rb-ACE	LGWPQYTWTPN-----
	** * * *
ace-2	PKNVSDIIPRTEVEKAIRMSRSRINDAFRLNDNSLEFLGIOPTLGPPNQPVSITWLIIVFG TMD
hu-ACET	-----SARSE-----GPLPDSGRVS-----FLGLDLD---AQQARVGQWLLLFL
mu-ACET	-----TARAE-----GSTAESNRVN-----FLGLYLE---PQQARVGQWVLLFL
rb-ACET	-----SARSE-----GSLPDSGRVN-----FLGMNLD---AQQARVGQWVLLFL
hu-ACE	-----SARSE-----GPLPDSGRVS-----FLGLDLD---AQQARVGQWLLLFL
mu-ACE	-----TARAE-----GSTAESNRVN-----FLGLYLE---PQQARVGQWVLLFL
rat-ACE	-----TARAE-----GSLPDSGRVN-----FLGMNLD---PQQARVGQWVLLFL
rb-ACE	-----SARSE-----GSLPDSGRVN-----FLGMNLD---AQQARVGQWVLLFL
	.*: * . : : * : : * : : * : : *
ace-2	VVMGVIVVGIVILIFTGIRDRKKKNKARSGENPYASIDISKGENNPGFONTDDVQTSFN
hu-ACET	GIALLVATLGLSQRLFSIR-HRSLHRHSHG-----PQFGSEVELRHS--
mu-ACET	GVALLVATVGLAHRLYNIRNHHSLRRPHRG-----PQFGSEVELRHS--
rb-ACET	GVALLLASLGLTQRLFSIR-YQSLRQPHHG-----PQFGSEVELRHS--
hu-ACE	GIALLVATLGLSQRLFSIR-HRSLHRHSHG-----PQFGSEVELRHS--
mu-ACE	GVALLVATVGLAHRLYNIRNHHSLRRPHRG-----PQFGSEVELRHS--
rat-ACE	GVALLVATVGLAHRLYNIRNHHSLRRPHRG-----PQFGSEVELRHS--
rb-ACE	GVALLLASLGLTQRLFSIR-YQSLRQPHHG-----PQFGSEVELRHS--
	: : : : : * : : * : : *

Fig. 2D

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HUM_tACE -----
HUM_ACE   MGAASGRRGPGLLLPLPLLLLLLPPQPALALDPGLQPGNFSADEAGAQLFAQSYNSSAEQV
DROME_ACE -----
ace-2     -----
CE_ACE    -----

HUM_tACE -----
HUM_ACE   LFQSVAAASWAHDTNITAENARRQEEAALLSQEFABANGQKAKELYEPIWQNFDPQLRRI
DROME_ACE -----
ace-2     -----
CE_ACE    -----

HUM_tACE -----
HUM_ACE   IGAVRTLGSANLPLAKRQQYNALLSNMSRIYSTAKVCLPNKTATCWSLDPDLTNILASSR
DROME_ACE -----
ace-2     -----
CE_ACE    -----

HUM_tACE -----
HUM_ACE   SYAMLLFAWEGWHNAAGIPLKPLYEDFTALSNEAYKQDGFTDTGAYWRSWYNSPTFEDDL
DROME_ACE -----
ace-2     -----
CE_ACE    -----

HUM_tACE -----
HUM_ACE   EHLYQQLEPLYLNLBAFVRRALHRRYGDRYINLRGPIPAHLLGDMWAQSWENIYDMVVPF
DROME_ACE -----
ace-2     -----
CE_ACE    -----

HUM_tACE -----
HUM_ACE   PDKPNLDVTSTMLQOGWNATHMFRVAEEFETSLELSPMPPEFWEGSMLEKPADGREVVCH
DROME_ACE -----
ace-2     -----
CE_ACE    -----

HUM_tACE -----
HUM_ACE   ASAWDFYNRKDFRIKQCTRVTMDQLSTVHEMGGHIQYYLQYKDLVSLRRGANPGFHEAI
DROME_ACE -----
ace-2     -----
CE_ACE    -----

HUM_tACE -----
HUM_ACE   GDVLALSVATPEHLHKIGLLDRVNTDTESDINYLLKMALEKIAFLPFGYLVQWRWGVFS
DROME_ACE -----
ace-2     -----
CE_ACE    -----MKFHILLLLLV

HUM_tACE -----
HUM_ACE   GRTPPSRYNFDWWYLRTKYQGICPPVTRNETHFDAGAKFHVPNVTPYIRYFVSFVLQFQF
DROME_ACE -----
ace-2     -----
CE_ACE    GACLPVFTQEIKPKPELLPADEAPKDPEAVFSEGEPPFELTDALDTPKNGSVPVPEPEPKP
```

Fig. 3A

8/23

```
HUM_tACE -----MGQGWATAGLPSSLFLLLCYGHPLL
HUM_ACE  HEALCKEAGYEGPLHQCDIYRSTKAGAKLRKVLQAGSSRPWQEVKDMVGLDALDAQPLL
DROME_ACE -----
ace-2    -----
CE_ACE   EPEPEPEPKPEPEPSPTPEPEPAIKFDNIESEDYGDVAETAASTQPDENTEVIEQLVDT

HUM_tACE VPSQEASQQVTVTEHGTSSQATTSSQTTTHQATAHQTSAQSPNLVTDEAEASKFVEEYDRT
HUM_ACE  KYGQPVTVQWLQEQNQNGEVLGWPEYQWHPPLPDNYPEG-IDLVTDAAEASKFVEEYDRT
DROME_ACE -----MRLFLALLATLAVTQALVKEEIQAKEYLENLNKE
ace-2    -----MSSSSWLLLSLVAVTAAQSTIEEQAKTFLDKFNHE
CE_ACE   FLNTGSIASNKTNKGPVFANPVAQALVNSSNYWKTDLNLAQPGSIKDEEKLRSWLAGYEAE
               . * : : :

HUM_tACE SQVWNEYAEANWNYNTNITTTETSKILLQKNMQLANHTLKYGTQARKFDVNQLQNTTIKR
HUM_ACE  SQVWNEYAEANWNYNTNITTTETSKILLQKNMQLANHTLKYGTQARKFDVNQLQNTTIKR
DROME_ACE LAKRTNVETEAAWAYGSNITDENEKKKNEISAEIAKFMKEVASDITTKFQWFSYQSEDILKR
ace-2    AEDLFYQSSLASWNYNTNITEENVQNMNAGDKWSAFLKEQSTLAQMYPLQEIQLNLTVKL
CE_ACE   AIKVLREVALSGWRYFNDASPSLKLALDEAENVLTMPVVRSTSMQAKQFDMASVTDEKVMR
               : : * * . : : . : : . : : . : :

HUM_tACE IIKKVQDLERAALPAQEELEYNKILLDMETTSVATVCHPNGS---CLQLEPDLTNVMAT
HUM_ACE  IIKKVQDLERAALPAQEELEYNKILLDMETTSVATVCHPNGS---CLQLEPDLTNVMAT
DROME_ACE QFKALTKLGYAALPEDDYAELLDTLSAMESNFAKVKVCYKDKSTKCDLALDPEIEEVISK
ace-2    QLOALQONGSSVLSEDKSKRLNTILNTMSTIYSTGKVCNPDNPQE-CLLLEPGLNEIMAN
CE_ACE   QLGYSFEGMSALAPSRFADYSQAQAALNRDSKSTICDKDVPPP-CALQKIDMDSIFRN
               : : : * . . : : . : * . . . : : :

HUM_tACE SRKYEDLLWAWEGWRDKAGRAILOFYPKYVELINQAARLNGYVDAGDSWRSMYETP----
HUM_ACE  SRKYEDLLWAWEGWRDKAGRAILOFYPKYVELINQAARLNGYVDAGDSWRSMYETP----
DROME_ACE SRDHEELAYYWREFYDKAGTAVRSQFERYVELNTRAAKLNNFTSGAEAWLDEYEDD----
ace-2    SLDYNERLWAWESWRSEVGKQLRPLYEYVVLKNEMARANHYEDYGDYWRGDYEVNGVDG
CE_ACE   EKDASRLQHLWVSVTAIAKSK-PSYNNIITISNEGAKLNGFANGGAMWRSADFMS--K
               . . . * : . : : : : * : * : . . * . : :

HUM_tACE -----SLEQDLERLFQELQPLYLNLHAYVRRALHRHYG-AQHINLEGPIPAHLLGNMWA
HUM_ACE  -----SLEQDLERLFQELQPLYLNLHAYVRRALHRHYG-AQHINLEGPIPAHLLGNMWA
DROME_ACE -----TFEQQLEDIFADIRPLYQQIHGYVFRRLRKHYG-DAVVSETGPIPMHLLGNMWA
ace-2    YDYSRGLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAY--PSYISPIGCLPAHLLGDMWG
CE_ACE   VHKAEFDLNKQIDKIYSTIQPFYQLLHAYMRRQLAGIYSNPVGLSKDGPPIPAHLFGSLDG
               : : : : : : : * * * * * : . * * * * : :

HUM_tACE QTWSNIYDLVVPFPPSA--PSMDTTEAMLKQGWTPRRMFKEADDDFTSLGLLPVPPEFWNK
HUM_ACE  QTWSNIYDLVVPFPPSA--PSMDTTEAMLKQGWTPRRMFKEADDDFTSLGLLPVPPEFWNK
DROME_ACE QQWSEIADIVSPFPEK--PLVDVSAEMEKQAYTPLKMFQMGDDFTSMNLTKLPQDFWDK
ace-2    RFWTNLYSLTVPFQOK--PNIDVTDAMVDQAWDAQRIFKEAEKFFVSVGLPNMTQGFWEN
CE_ACE   GDWSAHYEQTKPFEESETPPEAMLSAFNTQNYTTKMFVTAYRYFKSAGFPPLPKSYWTS
               * : . . * * . : : * : . : * * : : * :

HUM_tACE SMLEKPTDGREVVCHAS-AWDFYNGKDFRIKQCTTVNLEDLVVAHHEMGGHIQYFMQYKDL
HUM_ACE  SMLEKPTDGREVVCHAS-AWDFYNGKDFRIKQCTTVNLEDLVVAHHEMGGHIQYFMQYKDL
DROME_ACE SIIEKPTDGRDLVCHAS-AWDFYLIDDVRIKQCTRVTDQDLFTVHHELGHIQYFLQYQHQ
ace-2    SMLTDPGNVQKAVCHPT-AWDLGKG-DFRIIMCTKVMTDDFLTAAHHEMGGHIQYDMAYAAQ
CE_ACE   SIFAR-VWSKDMICHPAALDMRAPNDFRVKACAQLGEPDFEQAHSLLVQTYQYLYKDQ
               * : : : * * : * * : * : : : * : : *

HUM_tACE PVALREGANPGFHEAIGDVLALSVSTPKHLESNLLSSEGGSD--EHDINFLMKMALDKI
HUM_ACE  PVALREGANPGFHEAIGDVLALSVSTPKHLESNLLSSEGGSD--EHDINFLMKMALDKI
DROME_ACE PFVYRTGANPGFHEAVGDVLSLSVSTPKHLEKIGLLKDYVRDD--EARINQLFLTALDKI
ace-2    PFLLRNGANEGFHEAVGEIMSLSAATPKHLKSIGLLSPDFQEDN-ETEINFLKQALTIV
CE_ACE   SLLFREQASPVITDAIANAFALSTNPHYLYSQKLVPSEHLDIKDSVIINKLYKESLESF
               . . * * . : : : : : : : * : . . * * : *
```

Fig. 3B

9/23

HUM_tACE AFIPFSYLVDQWRWRVFDGSITKENYNQEWWSLRLKYQGLCPPVPRTQGD FPGAKFHIP
HUM_ ACE AFIPFSYLVDQWRWRVFDGSITKENYNQEWWSLRLKYQGLCPPVPRTQGD FPGAKFHIP
DROME_ ACE VFLPFAFTMDKYRWSLFRGEVDKANWNCAFWKLRDEYSGIEPPVVRSEKDFDAPAKYHIS
ace-2 GTLPFTYMLEKWRWMVFKGEIPKDQWMKKWEMKREIVGVVEPVPHDETYCDPASLFHVS
CE_ ACE TKLPFTIAADNWRYE LFDGTVPKNKLNDRWWEIRNKYEGVRSPQPYNTSNLDALIHNSVS
: ** : : : : : * : : : : : * : : : : : *

HUM_tACE -SSVPYIRYFVSFIIQFQFHEALCQAAGHTG-----PLHKCDIYQSKEAGORLATAMKL
HUM_ ACE -SSVPYIRYFVSFIIQFQFHEALCQAAGHTG-----PLHKCDIYQSKEAGORLATAMKL
DROME_ ACE -ADVEYLRYLVSFIIQFQFYKSACIKAGQYDPDNVELPLDNCDIYGSARAGAAFNMLSM
ace-2 -NDYSFIRYYTRTLYQFQFQEALCQAAGHTG-----PLHKCDISNSTEAGOKLFNMLRL
CE_ ACE QVHSPATRTLISYVLKFQILKALCQRELFWL-----SEGCTLSEDTT---EKLRETMKL
* : : ** : : * : : : : : : : : : : :

HUM_tACE GFSRPWPEAMQLITGQPNMSASAMLSYFKPLLDWLRTN-----
HUM_ ACE GFSRPWPEAMQLITGQPNMSASAMLSYFKPLLDWLRTN-----
DROME_ ACE GASKPWPDALEAFNGERIMSGKATAEYFEPLRVWLEAEN-----
ace-2 GKSEPWTALLENVVGAKNMNVRPLLNYFEPLFTWLKDQNKNSFVGWSTDWSPYADQSIKV
CE_ ACE GSSITWLKALEMISGKGELDAQPLLEYEPLINWLRTN-----
* * . * * : : . * : . : . : * * * . *

HUM_tACE -ELHGEKLGWPOYNWTPNSAR-----
HUM_ ACE -ELHGEKLGWPOYNWTPNSAR-----
DROME_ ACE -IKNNVHIGWTTSNKCVSS-----
ace-2 RISLKSALGDKAYEWNNDNEMYLFRRSSVAYAMROYFLKVKNQMILFGEEDVRVANLKPRIS
CE_ ACE -EIDQVVVGWDGEGTPTFTVEEIPKTRQPGDGGNGLPSEDRVAFPGGE-----
: *

HUM_tACE -----SEGPLPDSGRVSFLGLDLDAQQARVG-----Q
HUM_ ACE -----SEGPLPDSGRVSFLGLDLDAQQARVG-----Q
DROME_ ACE -----
ace-2 FNFFVTAPKNVSDIIPRTEVEKAIRMSRSRINDAFRLNDNSLEFLGIQPTLGPPNQPPVS
CE_ ACE -----CVNGQECLLD SHCNGTICVCNDGLYTTLEIGNTFN---CVPGN

HUM_tACE WLLLFLGIALLVATLGLSQRLFS-IRHR-----SLHRHSHGPQFGSEVE
HUM_ ACE WLLLFLGIALLVATLGLSQRLFS-IRHR-----SLHRHSHGPQFGSEVE
DROME_ ACE -----
ace-2 IWLIVFGVVMGVIVVGIVILIFTGIRDRKKKNKARSGENPYASIDISKGENNPGFQNTDD TMD
CE_ ACE PADSGFGDGKGLVIGLDFNNEVTTPEPSAEPEP--TAKTTTKMPPRVRAATSPFSLYLTV

HUM_tACE LRHS----
HUM_ ACE LRHS----
DROME_ ACE -----
ace-2 VQTSFN--
CE_ ACE LLIIFYAL

Fig. 3C

10/23

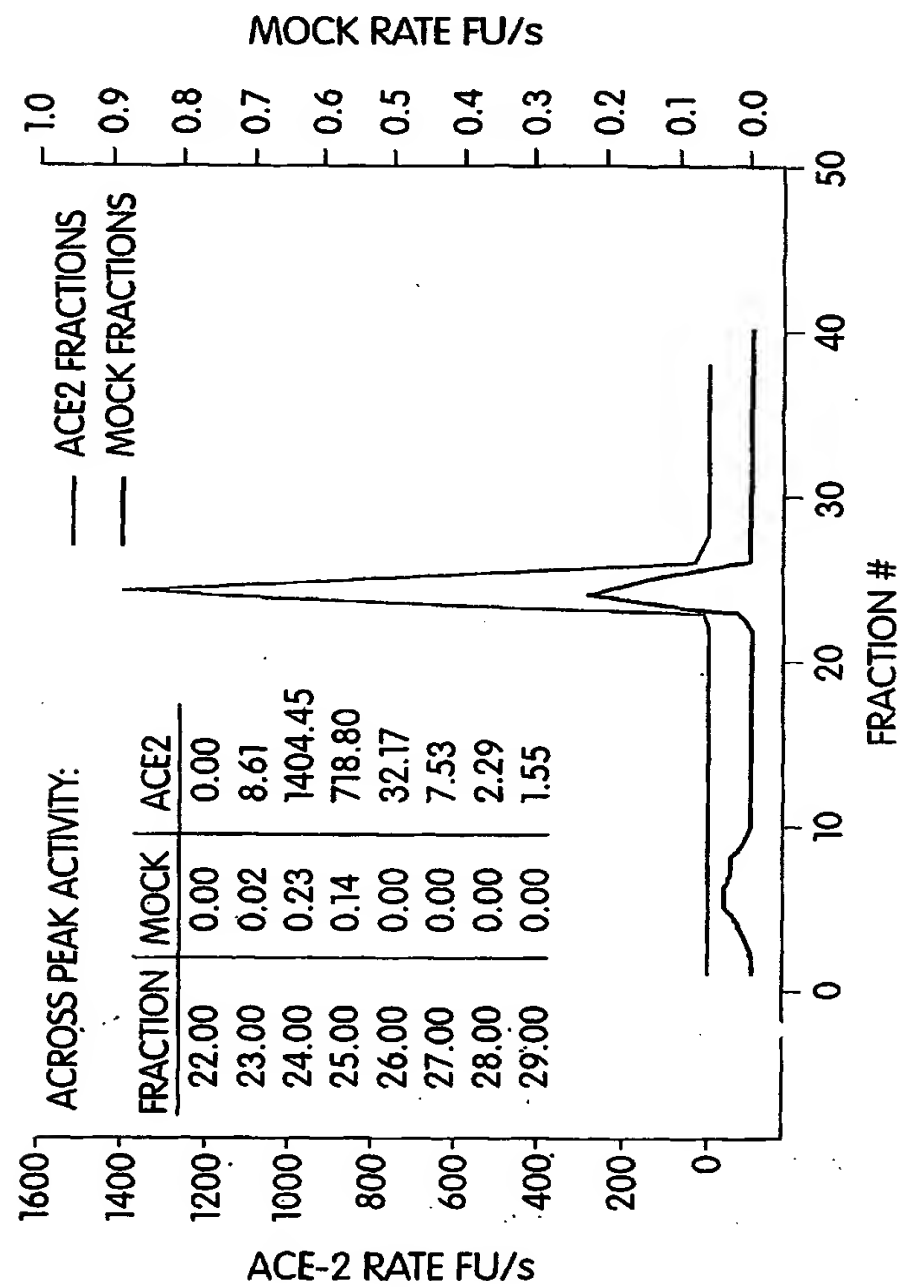


Fig. 4

11/23

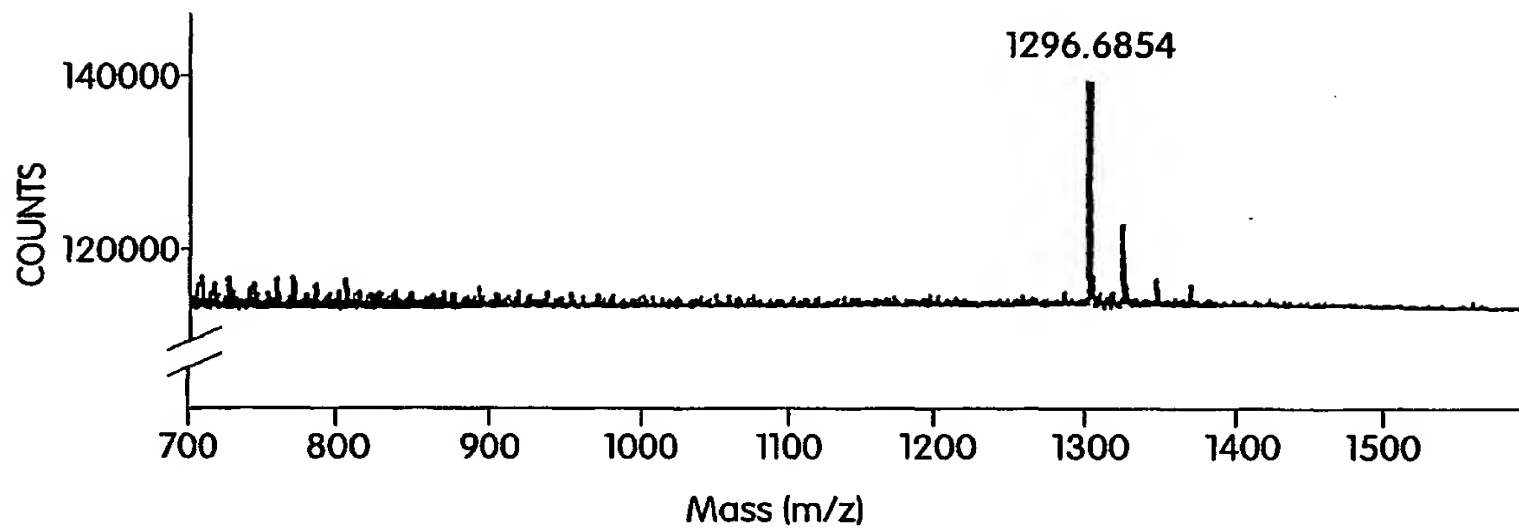


Fig. 5A

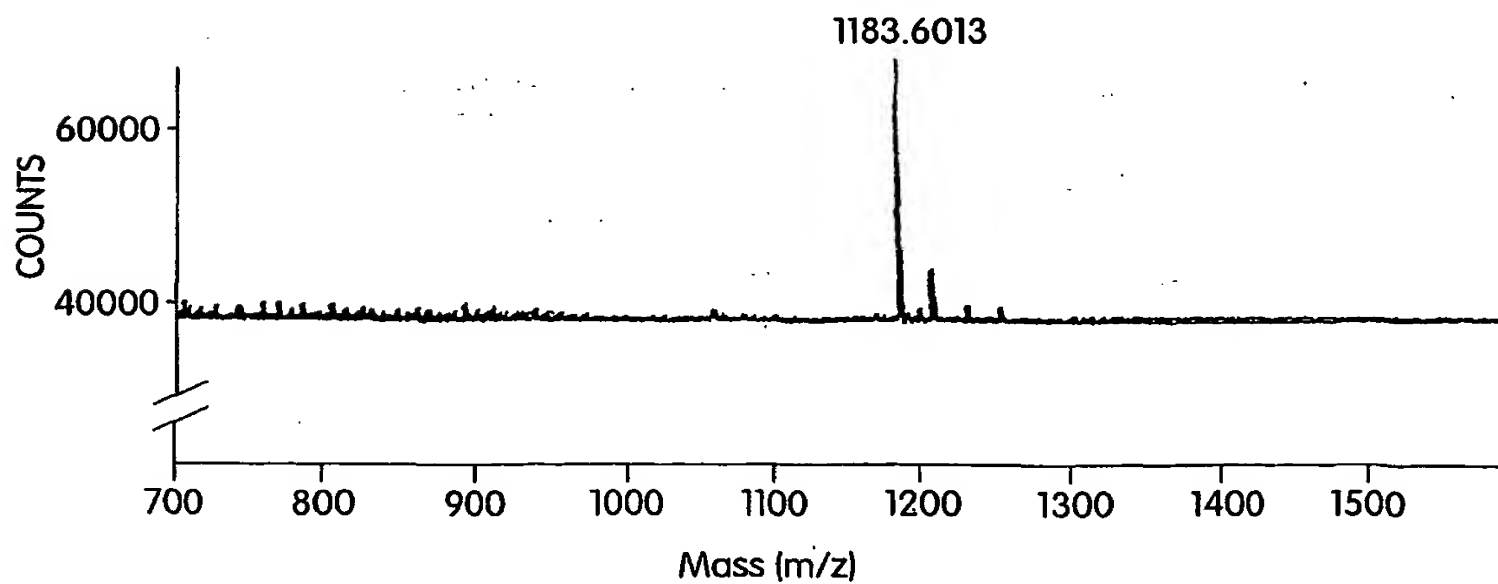


Fig. 5B

12/23

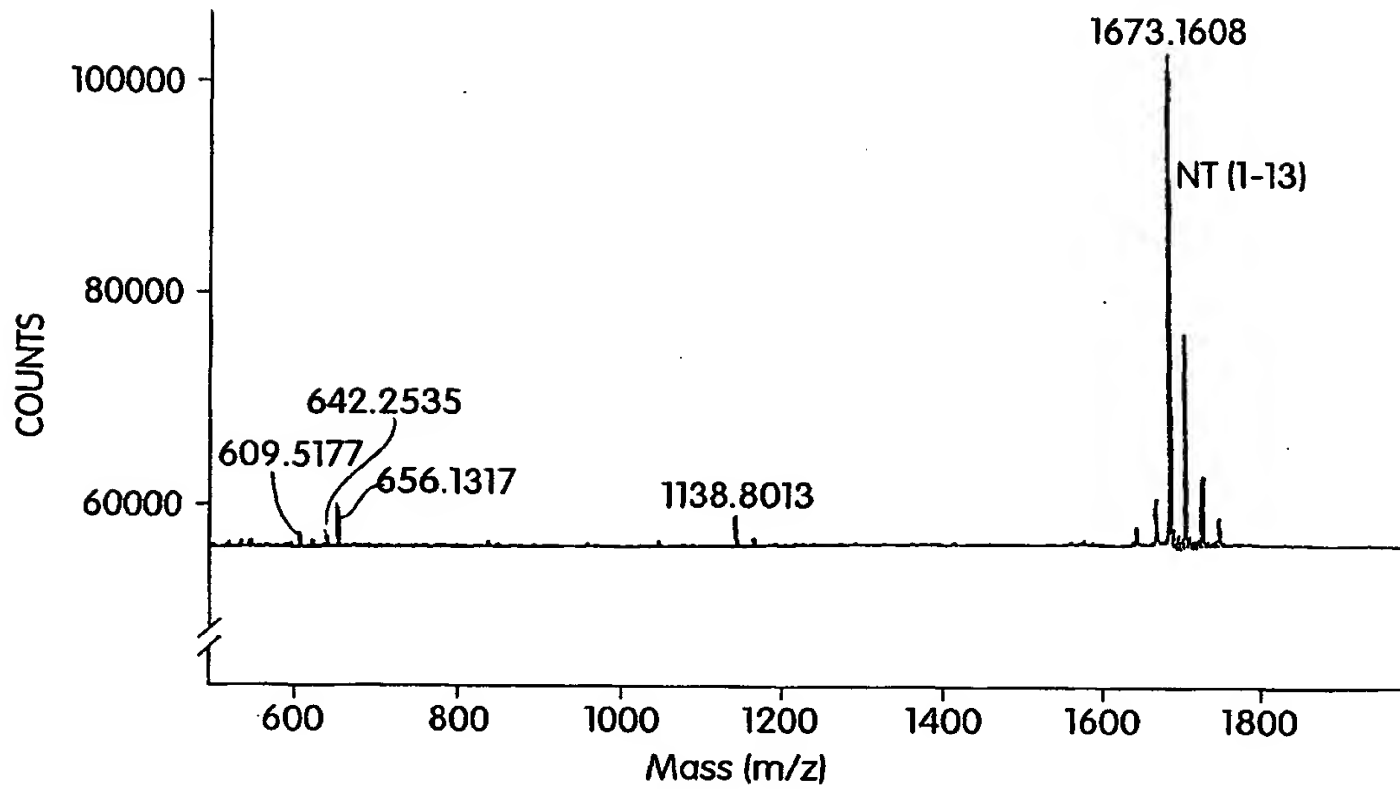


Fig. 6A

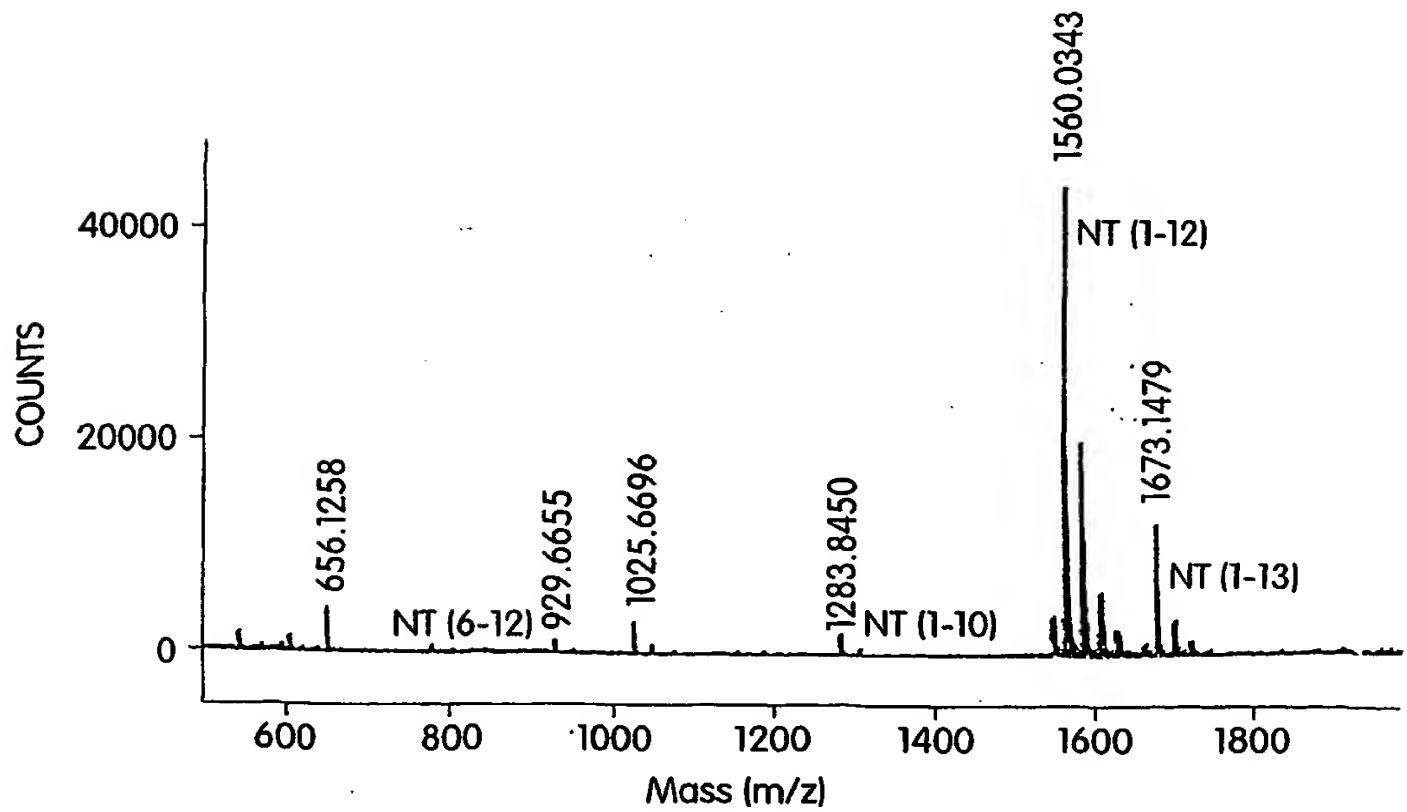


Fig. 6B

13/23

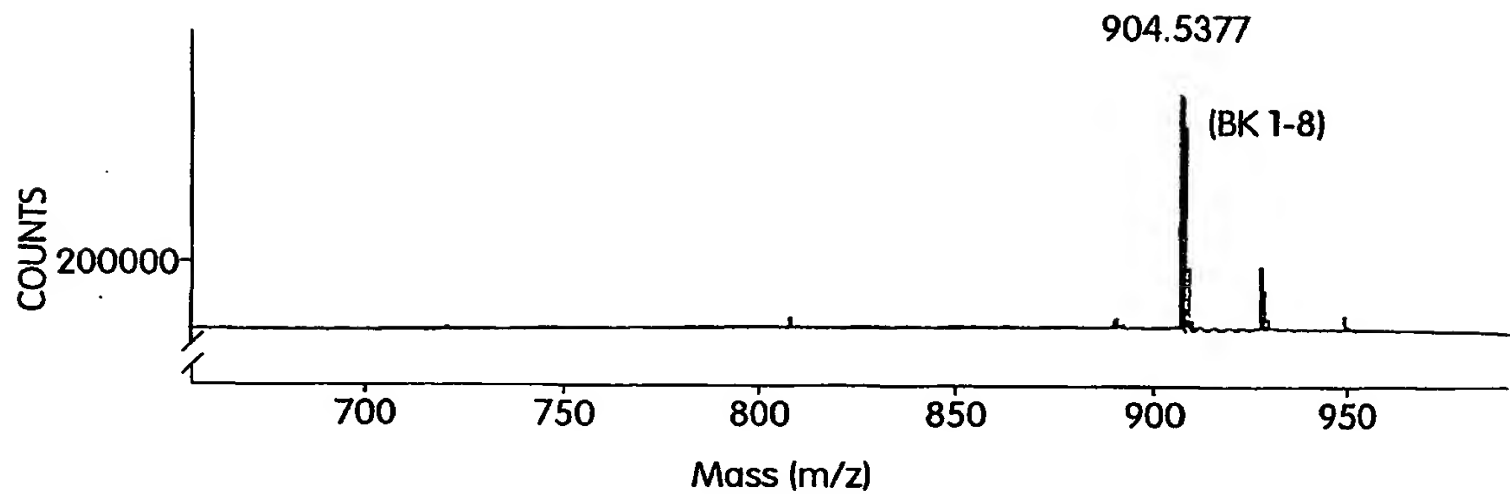


Fig. 7A

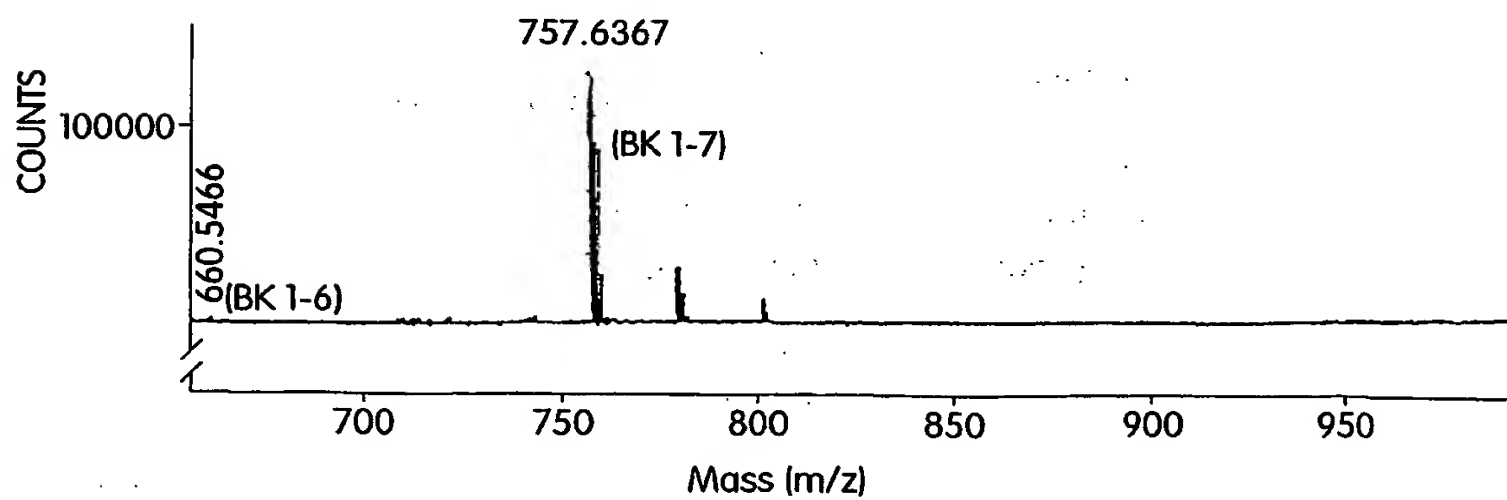


Fig. 7B

14/23

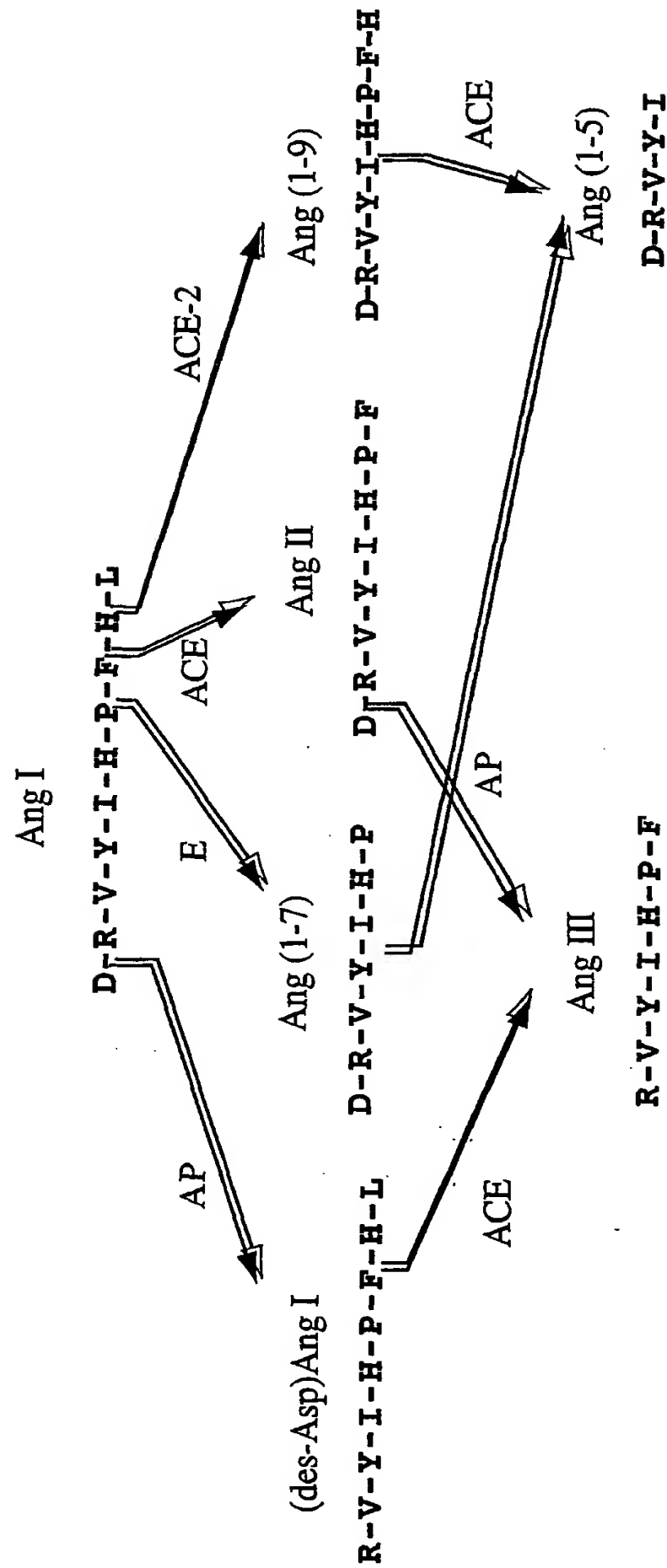
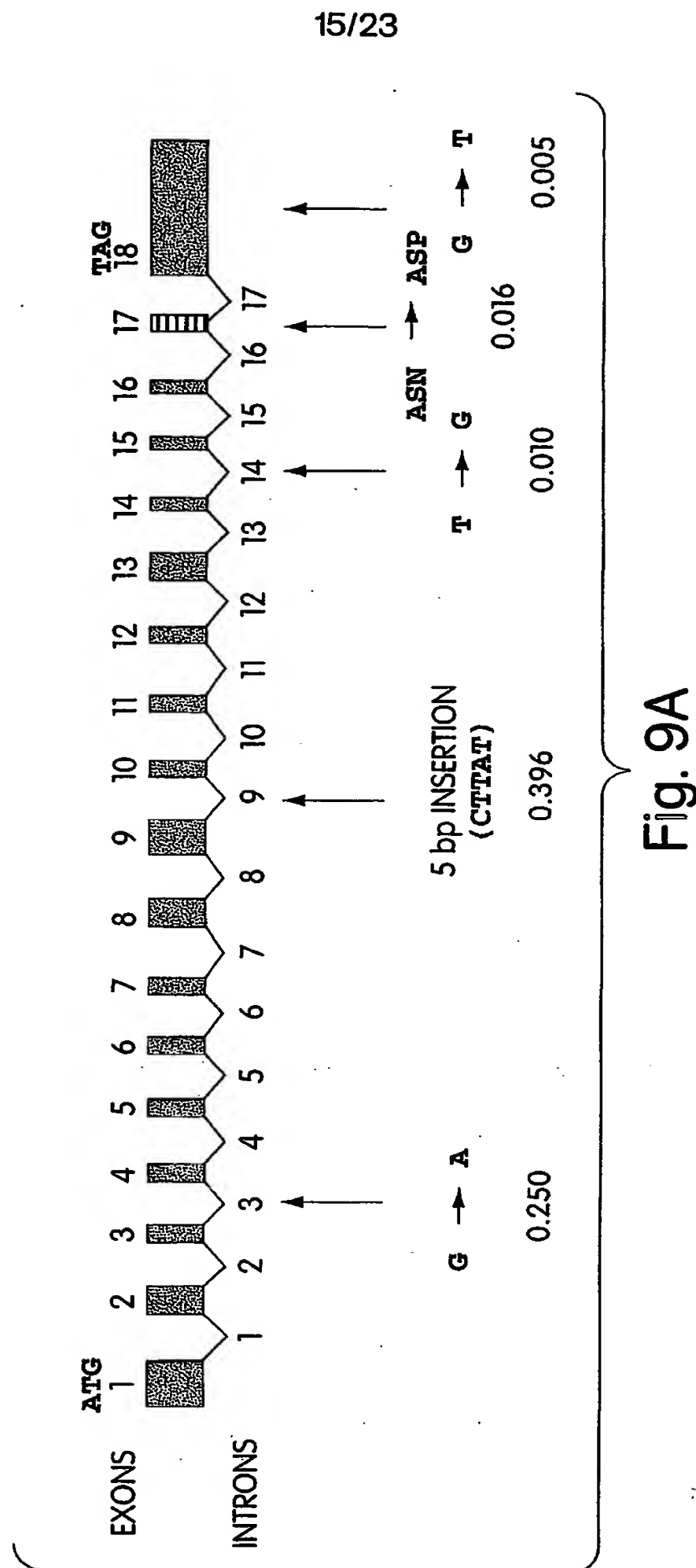


Fig. 8



16/23

GAATTCGGCTTCCATCCTAATACGACTCACTATAGGGCTCGAGCGGCGCCCGGGGCGAGGTATCTTGGCTCACAGGGGACGATGTCAAG
CTCTTCCTGGCTCCTTCTCAGCCTTGTGCTGTAACTGCTGCTCAGTCCACCAATTGAGGAACAGGCCAAGACATTTTGGACAAGTTAAC
CACGAAGCCGAAGACCTGTTCTATCAAAGTTCACTTGGCTTCTTGGAAATTATAACACCAATATTAAGTGAAGAGAATGTCCAAAACAT /
GAATAATGCTGGGGACAAATGGTCTGCCCTTTTAAAGGAACAGTCCACACTTGGC
CAAATGTATCCACTACAAGAAATTCAGAATCTCAGTCAAGCTTCAGCTGCAGGCTCTTCAGCAAAATGGGTCTTCAGTGTCTCAGAA
GACAAGAGCAAACCG / TTGAACACAATTCTAAAT

G-A INTRONIC
3a/3b

ACAATGAGCACCATCTACAGTACTGGAAAAGTTTGAACCCAGATAATCCACAAGAATGCTTATTACTTGAACCAGG /
TTTGAATGAAATAATGGCAACAGTTTAGACTACAATGAGAGGCTCTGGGC
TTGGGAAAGCTGGAGATCTGAGGTCCGCAAGCAGCTGAGGCCATTATATGAAGAGTATGTGGTCTTGAAAAATGAGATGGCAAGAGCAA
ATC / ATTATGAGGACTATGGGGATTATGGAGAGGAG
ACTATGAAGTAAATGGGGTAGATGGCTATGACTACAGCCGCGCCAGTTGATTGAAGATGTGGAACATACCTTTGAAGAG /
ATTAAACCATTAATGAACATCTTCATGCCCTATGTGAGGGC
AAAGTTGATGAATGCCATCTCTTCTATATCAGTCCAATTGGATGCCCTCCCTGCTCATTGCTTGG /
TGATATGTGGGTAGATTTTGGACAAATCTGTACTCTTTGACAGTTCCTTTGGACAGAAA
CCAAACATCGATGTACTGATGCAATGGTGGACCAG / GCCTGGGATGCACAGAGAAATATT
CAAGGAGGCCGAGAAATCTTTGTATCTGTGGTCTTCTTAATGACTCAAGGATTCTGGGAAATTCATGCTAACGGACCCAGGAAA
TGTTCAAGAAAGCAGTCTGCCATCCACAGCTTGGGACCTGGG /
GAAGGGCGACTTCAGGATCCTTATGTGCACAAAGGTGACAATGGACGACTTCCTG
ACAGCTCATCATGAGATGGGGCATATCCAGTATGATATGGCATATGCTGCACAACCTTTTCTGCTAAGAAATGGAGCTAATGAAGGATTC
CATGAAGCTGTGGGAAATCATGTCACTTTCTGCAGCCACACCTAAGCATTTAAATCCATTGGTCTTCTGTCAACCGATTTCAGAAAG

5 bp INSERTION
(CTAT)

ACAATG / AAACAGAAATAAACTTCTGCTCAAACAAGCACTCAGGATTTGTTGGGACTCTGCCATTTACTTA
CATGTTAGAGAAGTGGAGGTGGATGGTCTTTAAAGGGGAAATTCCTAAAGACCAAGTGGATGAAAAAGTGGTGGGAGATGAAG /
CGAGAGATAGTTGGGGTGGTGAACCTGTGCCCATGATGAAA
CATACTGTGACCCCGCATCTCTGTCCATGTTTCTAATGATTACTCATTCAATCG / ATATTACA
CAAGGACCTTTTACCAAATTCAGTTTCAAGAAGCACTTTGTCAAGCAGCTAAACATGAAGGCCCT
CTGCACAAATGTGACATCTCAAACTCTACAGAAGCTGGACAGAACTG /
TTCAATATGCTGAGGCTTGGAAATCAGAACCCTGGACCTAGCATTGGAAATGTTGTAGGAGCAAGAACATGAATGTAAGGCCACT
GCTCAACTACTTTGAGCCCTTATTTACCTGGCTGAAAGACCAGAAACAAGAAATCTTTTGTGGGATGGAGTACCGACTGGAGTCC /
ATATGCAGACCAAAGCATCAAAGTGAGGATAAG

INTRONIC
9a/9b

CCTAAATCAGCTCTTGGAGATAAAGC / ATATGAATGGAACGACAATGAAATGTACC
TGTTCCGATCATCTGTTGCATATGCTATGAGGCAGTACTTTTAAAGTAAATAATCAGATGATTCTTTTGGG /
GAGGAGGATGTGGAGTGGCTAATTTGAAACCAAGAATCTCCTTTAATTTCTTT
GTCACCTGCACCTAAATATGTCTGATATCACTCTAGAACTGAAGTTGAAAGGCCATCAGG /
ATGTCCCGGAGCCGATCAATGATGCTTTCCGTCTGAATGACAACAGCCTAGAGTTCTGGG
GATACAGCCAACACTTGGACCTCCTAACAGCCCTGTTTCCATATGGCTGATTGTTTTTGGAGTTGTGATGGGAGTGATAGTGGTTGG
CATTGTCTCCTGATCTTCACTGGGATCAGAGATCGGAAGAAG /
AAAAATAAAGCAAGAAGTGGAGAAATCCTTATGCCTCCATCGATATTAGCAAAGGA
GAAATAATCCAGGATTCAAAACACTGATGATGTTGAGACCTCCTTTTAGAAAAATCTATGTTTTTCTCTTGGGTGATTTTGTGTATG
TAAATGTTAATTTTCAATGATAGAAAAATATAAGATGATAAGATATCATTAATGTCAAACTATGACTCTGTTTCAAAAAAATTTGTCCA
AAGACAACATGGCCAAGGAGAGAGCATCTTCATGACATTTGCTTTTCAATTTTCTGTCTGATTTGACTTCTGTTCTGTTCTTAA
TAAGGATTTTGTATTAGATATATTAGGGAAAGTGTGATTTGGTCTCACAGGCTGTTTCAAGGATAATCTAAATGTAAATGTCTGTTGAATT

T-G INTRONIC
14a/14b

A-G ASN-ASP
17c/17d

TCTGAAGTTGAAACAAAGATATATCATTTGGAGCAAGTGTGGATCTTGTATGGAATATGGATGGATCACTTGTAAAGACAGTGCCTGG
GAACGTGTGATGCTGCAAGGATTTGAGAATGGCATGCATTAGCTCACTTTTCAATTAATCCATTGTCAAGGATGACATGCTTTCTTCACAGTA
ACTCAGTTCAAGTACTATGGTATTTGCCCTACAGTGTGTTTGGAAATCGATCATGCTTTTCAAGGTGACAGGTCTAAAGAGAGAAGAAT
CCAGGGAACAGGTAGAGGACATTTGCTTTTCACTTCCAAGGTGCTTGTATCAACATCTCCCTGACAACACAAAAGTAGAGCCAGGGGCT
CCGTGAAGTCCCAGAGCATGCCGTATAGAACTCATTTTCTACTGTTCTTAACTGTGGAGTGAATGGAAATTCAACTGTATGTTCAACCT
CTGAAGTGGGTACCCAGTCTCTTAAATCTTTGTATTTGCTCACAGTGTGAGCAGTGTGAGCACAAGCAGACACTCAATAAATGCTA
GATTTACACTC / AAAAAAAAAAAAAAGGGCGGCCG

G-T 3'UTR
18e/18f

Fig. 9B

17/23

Bachem M-2195
Mca-Tyr-Val-Ala-Asp-Ala-Pro-Lys(Dnp)-OH
Caspase I (ICE) substrate

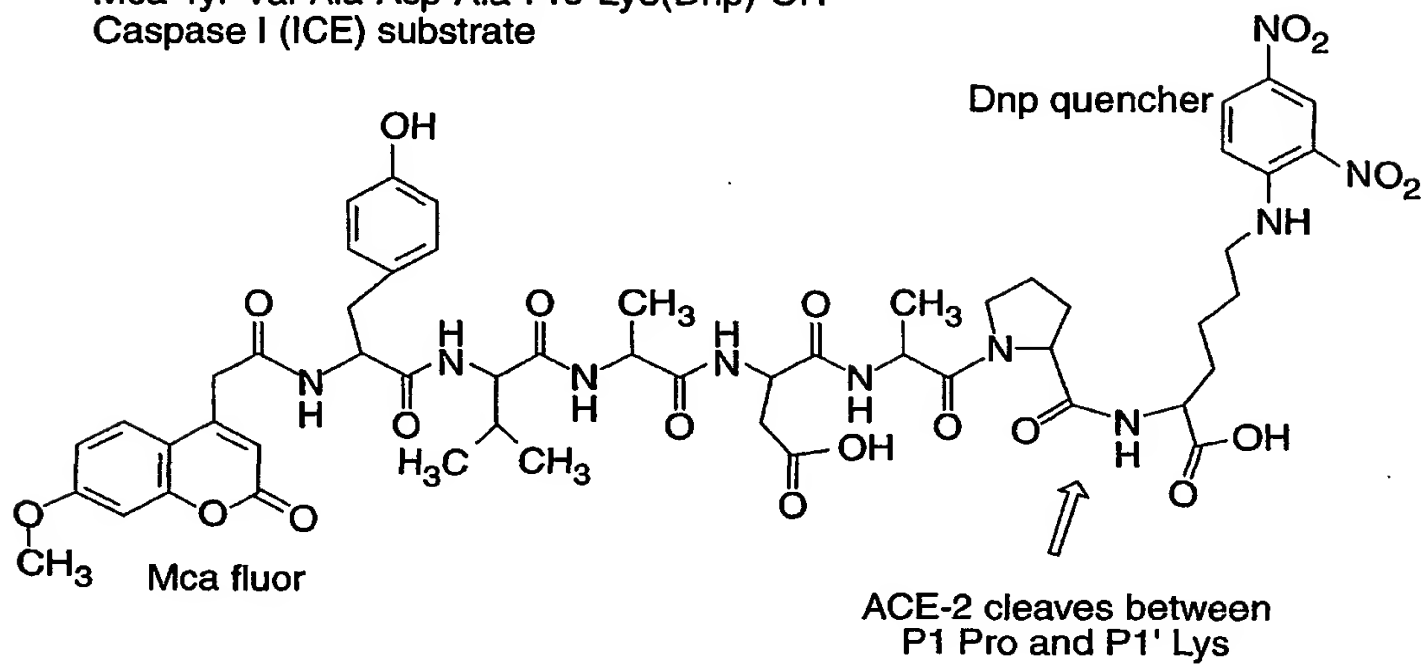


Fig. 10A

MIPH-1
custom synthesis (AnaSpec)
Mca-Ala-Pro-(Dnp)Lys-OH

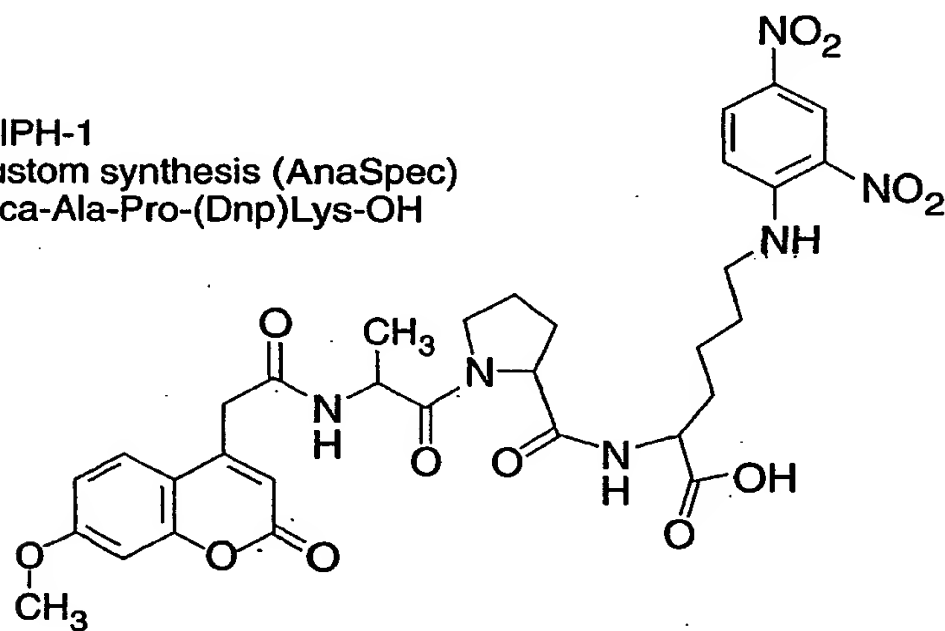


Fig. 10B

18/23

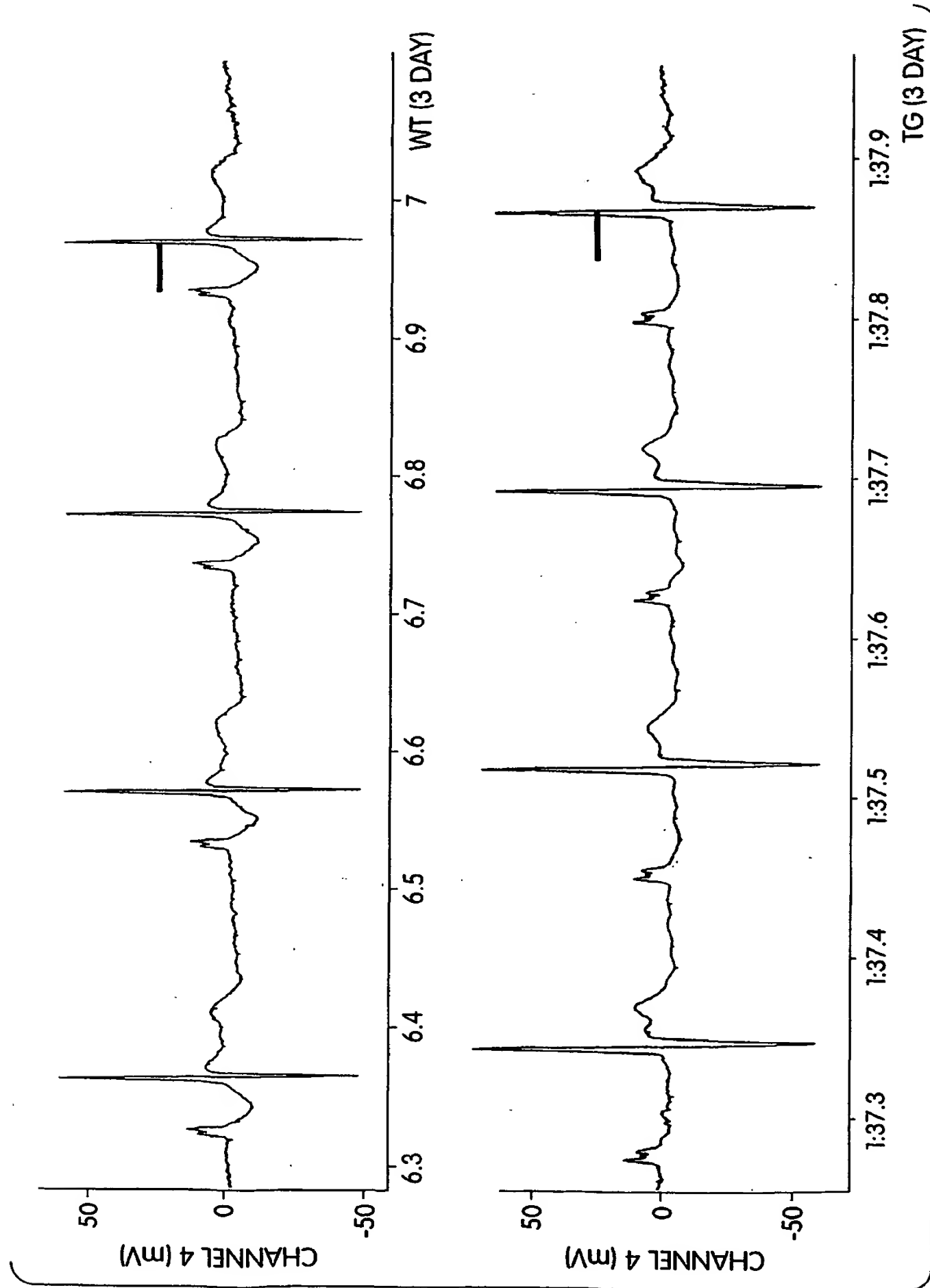


Fig. 11A

19/23

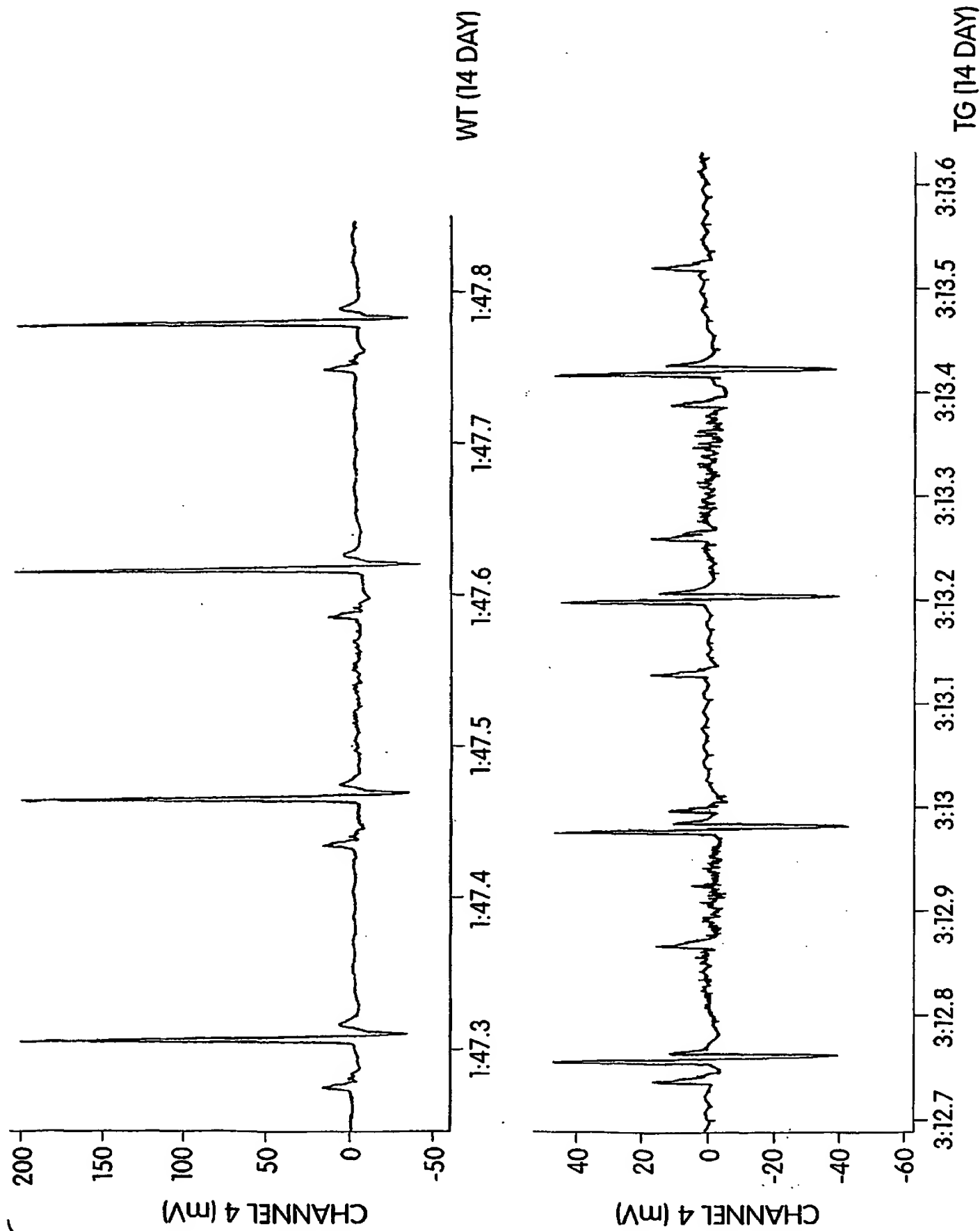


Fig. 11B

20/23

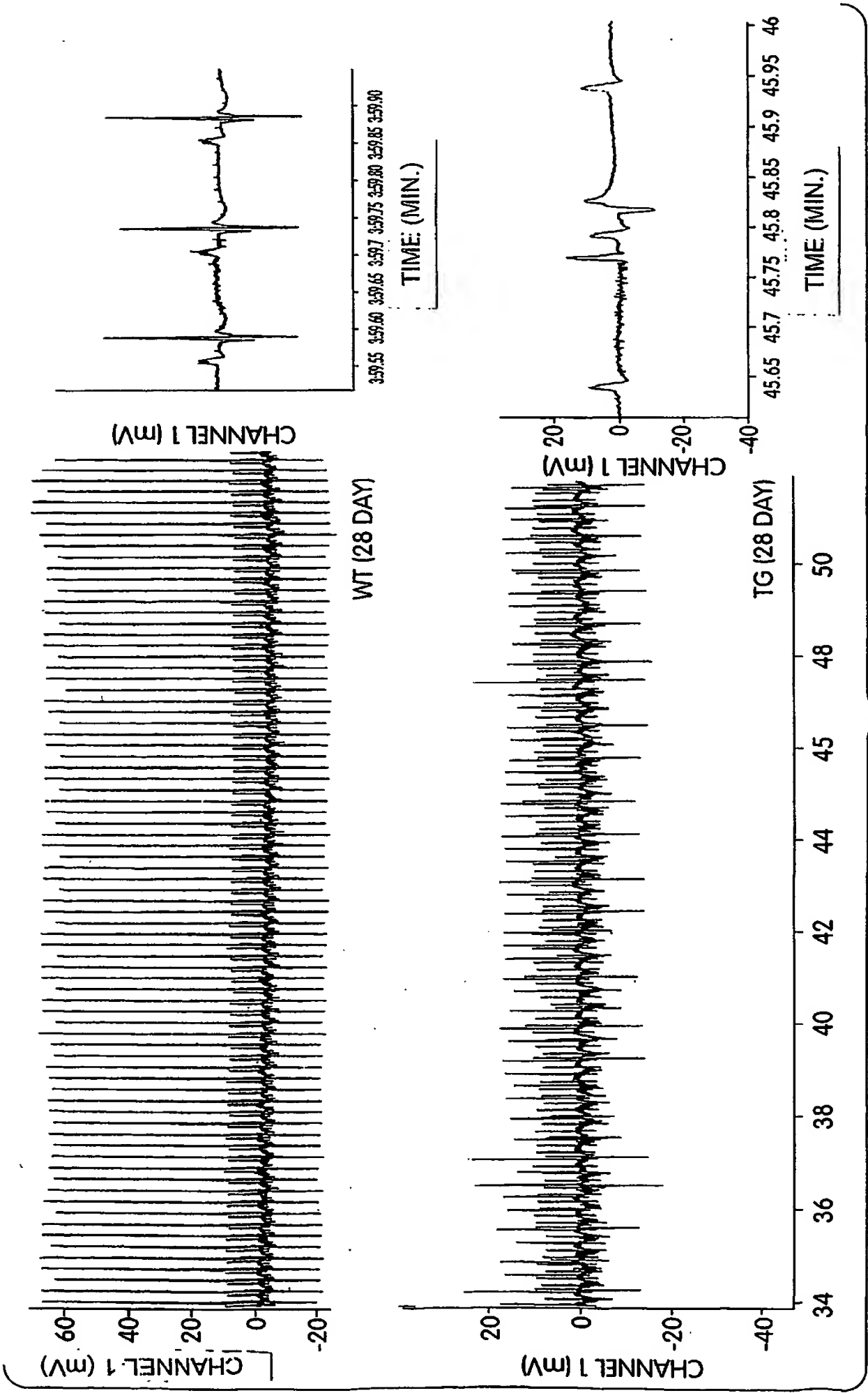


Fig. 11C

21/23

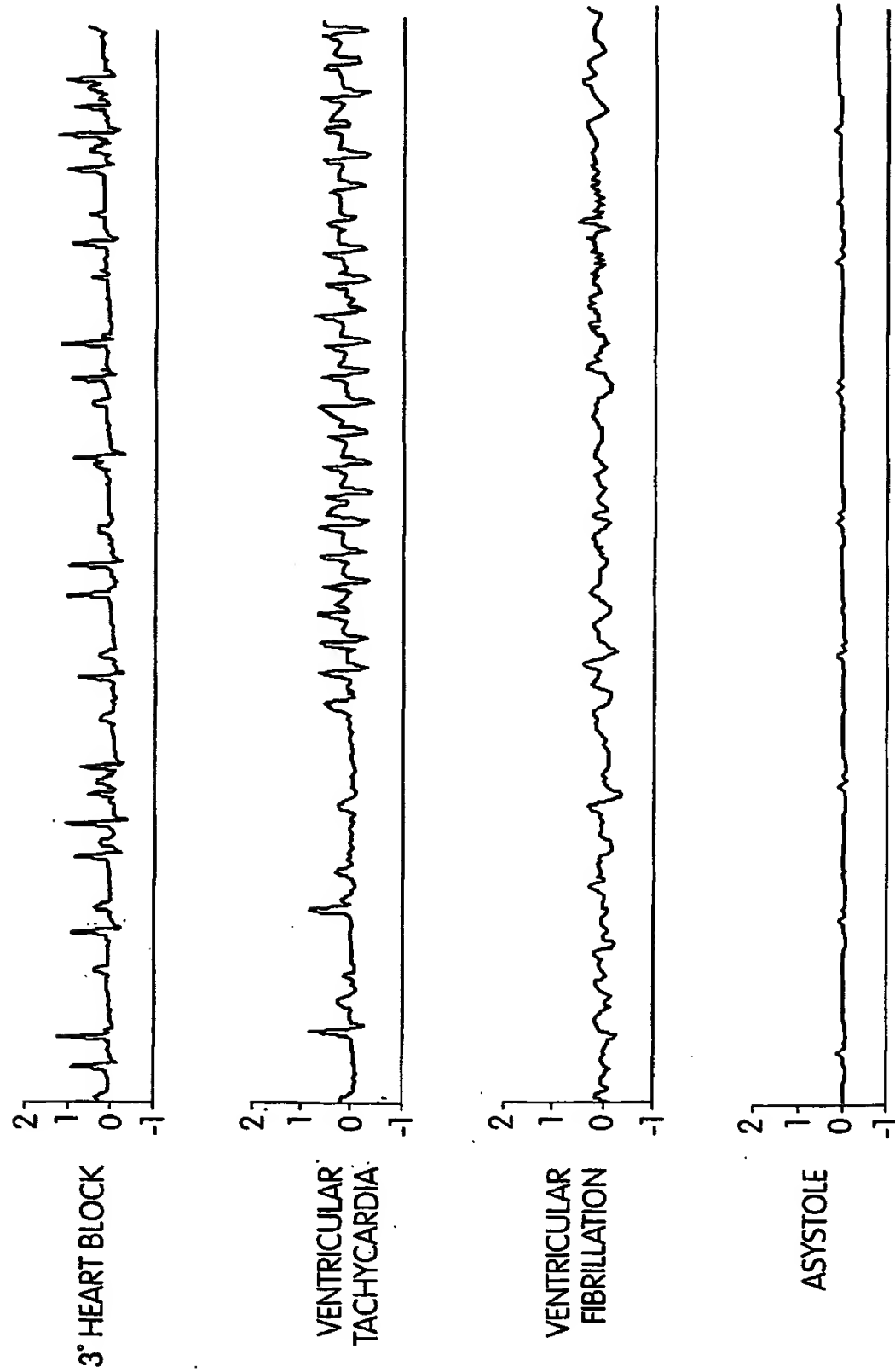


Fig. 12

22/23

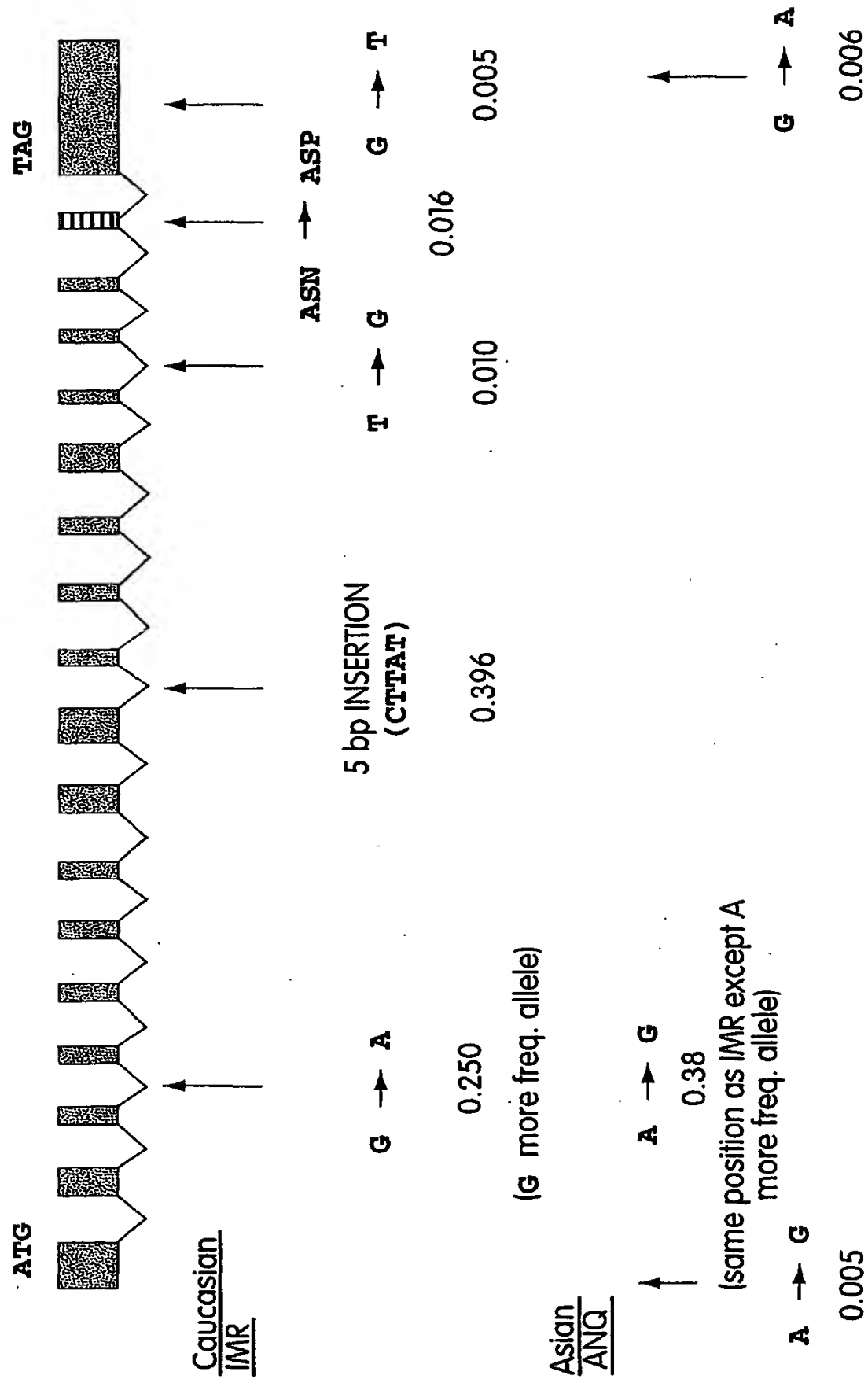


Fig. 13A

23/23

GAATTCGGCTTCCATCCTAATACGACTCACTATAGGGCTCGAGCGCCCGCCGGGGCAGGTATCTTGGCTCACAGGGGACGATGTCAG
CTCTTCCTGGCTCCTTCTCAGCCTTGTGCTGTAAGTCTGCTCAGTCCACCATTGAGGAACAGGCCAAGACATTTTGGACAAGTTTAAAC / A-G INTRONIC
CACGAAGCCGAAGACCTGTTCTATCAAAGTTCACCTTGCTTCTTGGGAATTATAACACCAATATTACTGAAGAGAATGTCCAAAACAT / 1c/1d
GAATAATGCTGGGGACAAATGGTCTGCCCTTTTAAAGGAACAGTCCACACTTGGC
CAAATGTATCCACTACAAGAAATTCAGAATCTCACAGTCAAGCTTCAGCTGCAGGCTCTTCAGCAAAATGGGTCTTCAGTGTCTCAGAA
GACAAGAGCAAACGG / TTGAACACAATTTCTAAAT G-A INTRONIC
ACAATGAGCACCATCTACAGTACTGGAAAAGTTTGTAAACCAGATAATCCACAAGAATGCTTATTACTTGAACCAGG / A-G INTRONIC
TTTGAATGAAATAATGGCAAACAGTTTACACTACAATGAGAGGCTCTGGGC 3a/3b
TTGGGAAGCTGGAGATCTGAGGTCGGCAAGCAGCTGAGGCCATTATATGAAGAGTATGTGGTCTTGA AAAATGAGATGGCAAGAGCAA
ATC / ATTATGAGGACTATGGGGATTATTTGGAGAGGAG
ACTATGAAGTAAATGGGTAGATGGCTATGACTACAGCCGCGGCCAGTTGATTGAAGATGTGGAACATACCTTTGAAGAG /
ATTAAACCATTTATATGAACATCTTCATGCCCTATGTGAGGGC
AAAGTTGATGAATGCCATCTCTTCTATATCAGTCCAATTGGATGCCCTCCCTGCTCATTGTGCTTGG /
TGATATGTGGGTAGATTTTGGACAAATCTGTACTCTTTGACAGTTCCTTTTGGACAGAAA
CCAAACATAGATGTTACTGATGCAATGGTGGACCAG / GCCTGGGATGCACAGAGAATATT
CAAGGAGGCCGAGAAGTTCTTTGTATCTGTTGGTCTTCTTAATATGACTCAAGGATCTGGGAAAATTCATGCTAACGGACCCAGGAAA
TGTTTCAGAAAGCAGTCTGCCATCCCACAGCTTGGGACCTGGG /
GAAGGGCGACTTCAGGATCCTTATGTGCACAAAGTGACAATGGACGACTTCCTG
ACAGCTCATCATGAGATGGGGCATATCCAGTATGATATGGCATATGCTGCACAACCTTTTCTGCTAAGAAATGGAGCTAATGAAGGATTG 5 bp INSERTION
CATGAAGCTGTTGGGAAATCATGTCACTTTCTGCAGCCACACCTAAGCATTTAAATCCATTGGTCTTCTGTCAACCGATTTTCAAGAAG (CTTAT)
ACAATG / AAACAGAAATAAACTTCTGCTCAAAACAAGCACTCACGATTTGTTGGGACTCTGCCATTTACTTA INTRONIC
CATGTTAGAGAAGTGGAGGTGGATGGTCTTTAAAGGGGAAATTCCAAAGACCACTGGATGAAAAAGTGGTGGGAGATGAAG / 9a/9b
CGAGAGATAGTTGGGGTGGTGAACCTGTGCCCATGATGAAA
CATACTGTGACCCCGCATCTCTGTTCCATGTTTCTAATGATTACTCATTCAATCG / ATATTACA
CAAGGACCTTTTACCAATTCAGTTTCAAGAAGCACTTTGTCAAGCAGCTAAACATGAAGGCCCT
CTGCACAAATGTGACATCTCAAACTCTACAGAAGCTGGACAGAACTG /
TTCAATATGCTGAGGCTTGGAAAATCAGAACCTGGACCTAGCATTGGAAAATGTTGTAGGAGCAAAGAATGAATGTAAGGCCACT
GCTCAACTACTTTTGGAGCCCTTATTTACCTGGCTGAAAGACCAGAACAGAAATCTTTTGTGGGATGGAGTACCGACTGGAGTCC /
ATATGCAGACCAAAGCATCAAAGTGAGGATAAG
CCTAAATCAGCTCTTGGAGATAAAGC / ATATGAATGGAACGACAATGAAATGTACC
TGTTCCGATCATCTGTTGCATATGCTATGAGGCAGTACTTTTAAAGGAAATTAATAATCAGATGATTCTTTTGGG /
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GTCAGTGCACCTAAAAATGTGTCTGATATCATTCTAGAACTGAAGTTGAAAAGGCCATCAGG /
ATGTCCCGGAGCCGTATCAATGATGCTTTCCGTCTGAATGACAAACAGCCTAGAGTTTCTGGG
GATACAGCCAAACACTTGGACCTCCTAACAGCCCCCTGTTTCCATATGGCTGATTGTTTTTGGAGTTGTGATGGGAGTGATAGTGGTTGG
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CTGAAGTGGGTACCCAGTCTCTTAAATCTTTTGTATTTGCTCACAGTGTGTTGAGCAGTGTGAGCACAAAGCAGACACTCAATAAATGCTA
GATTTACACACTC / AAAAAAAAAAAAAAGGGCGGCCCG

Fig. 13B